Methods: The yeast expression vectors of different spliceosomes and deletion mutants of CAML gene was constructed and transfected into yeast Y187, matching experiment with AH109 transfected pGBKT7-NS4A was performed. Diploid yeast was plated on synthetic dropout nutrient medium (SD/-Trp-Leu-His-Ade) containing X-α-gal.
Results: The yeast Y187 transfected with the yeast expression vectors of different spliceosomes and the mutants pGADT7/CAML-1–211 and pGADT7/CAML-1–57 of CAML gene could match successfully with AH109 transfected pGBKT7-NS4A, but pGADT7/CAML-58–211 and pGADT7/CAML-234–296 could not.
Conclusions: The interaction site of HCV NS4A and CAML located at the hydrophilic N-terminal 1–57 amino acid of CAML protein. All of the spliceosomes of CAML could bind with HCV NS4A.

PP-075 Seroprevalence of hepatitis C virus infection in Northern India and its association with blood groups, sex and age

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Background and Aims: Hepatitis C virus (HCV) infection is the major cause of post transfusion non-A, non-B hepatitis (NANB). In India scarcity of data exists for relationship between HCV infection and risk factors. Thus we evaluated the possible role of blood groups, age and sex in causing HCV infection.
Methods: A total of 20,000 blood donors, visiting GSVM Medical College, Kanpur, India were included in the present study. All the donors were subjected for anti-HCV antibodies detection by third generation Enzyme Linked Immunosorbent Assay (Anti-HCV ELISA 3.0, Span Diagnostics, Surat, India). Blood group of each donor was tested and the donors were categorized according to blood group, sex, age and correlated with risk factors. Statistical analysis was done by SPSS software version 11.5 (SPSS, Chicago, IL).
Results: Of the 20,000 study subjects, only 68 (0.34%) were HCV seropositive. The frequency of male individuals were similar in HCV seropositive group (98.52%) as compared to HCV seronegative group (96.16%; $p = 0.523$). Higher frequency of HCV seronegative subjects (30.32%) were found among 19–25 year age group as compared to HCV seropositive subjects (20.58%), however the difference is not significant ($p = 0.09$). Prevalence of individuals carrying AB blood group was higher in HCV seronegative group (10.18%) when compared with HCV seropositive group (1.47%) and was significantly associated with reduced susceptibility ($p = 0.014$).
Conclusions: Present study shows no association with age and gender. The possible role of blood group in causing HCV infection can not be ruled out.

PP-076 Screening of proteins binding to HCV E1 protein from human pancreas cDNA library by yeast two-hybrid

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Objective: To screen proteins of human pancreas cDNA library interacting with HCV E1 protein.
Methods: The library was amplifed, purified and evaluated, and then the puried library plasmids were transformed into yeast strain Y187. The reconstructed plasmid pGBKT7-E1 was transformed into yeast strain AH109 and screened on the nutrient deficiency medium SD/-Trp. The transformed AH109 mated with Y187 containing the library plasmid. The diploid yeast cells were plated on nutrient deficiency medium SD/-Trp/-Leu/-His/-Ade and SD/-Trp/-Leu/-His/-Ade containing X-α-gal for selecting. The plasmids in diploid yeast cells were extracted and electrotransformed into *E. coli* DH5α. The plasmids in DH5α were extracted, sequenced and analyzed by bioinformatic methods.
Results: Nine proteins interacting with HCV core were found.
Conclusions: These results show that HCV E1 protein may be related with metabolism of glucose and lipid.
Supported by the National Natural Science Foundation of China, No. 30600524.

PP-077 Screening of proteins binding to HCV core protein from human pancreas cDNA library by yeast two-hybrid

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Objective: To screen proteins of human pancreas cDNA library interacting with HCV core protein.
Methods: The library was amplified, purified and evaluated, and then the puried library plasmids were transformed into yeast strain Y187. The reconstructed plasmid pGBKT7-core was transformed into yeast strain AH109 and screened on the nutrient deficiency medium SD/-Trp. The transformed AH109 mated with Y187 containing the library plasmid. The diploid yeast cells were plated on nutrient deficiency medium SD/-Trp/-Leu/-His/-Ade and SD/-Trp/-Leu/-His/-Ade containing X-α-gal for selecting. The plasmids in diploid yeast cells were extracted and electrotransformed into *E.coli* DH5α. The plasmids in DH5α were extracted, sequenced and analyzed by bioinformatic methods.
Results: Eleven proteins interacting with HCV core were founded.
Conclusions: These results show that HCV core protein may be related with metabolism of glucose and lipid.
Supported by the National Natural Science Foundation of China, No. 30600524.

Poster Presentation – Late Submission

PP-078 Epidemiological investigation and analysis of Wuhan nosocomial infection of perianal surgical site infection in anorectal diseases

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Objectives: To investigate the Incidence of Wuhan nosocomial infection (NI) of surgical site infection (SSI) in anorectal diseases, and to conduct epidemiological analysis, in the establishment of "diagnostic criteria for NI of SSI in anorectal diseases" on the basis.
Methods: Epidemiological surveys method using prospective study, in Wuhan, the scale of five different hospitals surveys to collect information, and on the statistical method adopted anorectal diseases in-patients after the wound infection related factors such as age, sex, occupation, obesity, past history of disease and symptom, the duration of surgery, anesthesia, the incision site (including perianal) strains of bacteria and changes in hospital time and costs to carry out epidemiological analysis, and using the newly built "diagnostic criteria" to conduct of evaluation for NI of perianal SSI in anorectal diseases in Wuhan.